

## SEQUENCE LISTING

IAP20 Rec'd 16/07/2006  
R 2006

**SEQ ID 1 – NadA from strain 2996, with C-terminus deletion**

MKHFPSKVLTTAILATFCGALAATNDDVKAATVAIAAYNNQEIINGFKAGETIYDIDEDEGTITKKDATAA  
 DVEADDFKGLGLKKVVTNLTKVNENKQNVDAVKAAESEIEKLTTKLADTDAALADTAALDATTNALNKLGE  
 5 NITTFAEETKTNIVKIDEKLEAVADTVKHAEEAFNDIADSLENTKADEAVKTANEAKQTAEETKQNVDAVK  
 AAETAAGKAEEAAGTANTAAADKAEEAVAKVTDIKADIATNKDNIAKKANSADVYTREESDSKFVRIDGLNATTE  
 KLDTRLASAEKSIADHDTRLNLGKTVSDLRKETRQGLAEQAALSGLFQPYNVG

**SEQ ID 2 – NadA from strain 2996, with C-terminus deletion and leader peptide processed**

ATNDDVKAATVAIAAYNNQEIINGFKAGETIYDIDEDEGTITKKDATAADVEADDFKGLGLKKVVTNLTKV  
 10 NENKQNVDAVKAAESEIEKLTTKLADTDAALADTAALDATTNALNKLGENITTFAEETKTNIVKIDEKLEAV  
 ADTVDKHAEEAFNDIADSLENTKADEAVKTANEAKQTAEETKQNVDAVKAAETAAGKAEEAAGTANTAAADKA  
 EEEAVAKVTDIKADIATNKDNIAKKANSADVYTREESDSKFVRIDGLNATTEKLDTRLASAEKSIADHDTRLNL  
 GKTVSDLRKETRQGLAEQAALSGLFQPYNVG

**SEQ ID 3 – 4G741 from MC58 strain**

15 VAADIGAGLADALTAPLDHKDKGLQSLTLQSVRKNEKLKLAQGAEKTYGNQDSLNTGKLKNDKVSRFDFIRQ  
 IEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDFKLPPEGGRATYRG  
 AFGSDDAGGKLTYTIDFAAKQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEKGYSLSGIFGG  
 KAQEVAEKGSAEVKTVNGIRHIGLAQK

**SEQ ID 4 – 936 from MC58 strain with leader peptide processed**

20 VSAVIGSAAVGAKSAVDRRTGAQTDDNVMALRIETTARSYLRQNNQTKGYTPQISVVGVYNRHLLLQGVATEG  
 EKQFVGQIARSEQAAEGVNYITVASLPTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTVGMIL  
 TPEEQAQITQKVSTTVGVQKVITLYQNYVQR

**SEQ ID 5 – 953 from MC58 strain with leader peptide processed**

25 ATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKRDGKIDITIPIANLQSGSQHFTDHLKSADIFDA  
 AQYPDIFVSTKFNNGKKLVSDGNLTMHGKTAEPVLAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDFYL  
 VNVMGTMKSVRIDIQIEAAQK

**SEQ ID 6 – 4G287 from MC58 strain**

SPDVKSADTLSKPAAPVSEKETEAKEDAPQAGSQGQGAPSQGSQDMAAVSEENTGNGGAVTADNPKNEDVA  
 QNDMPQNAAGTDSSTPNHTPDPNMLAGNMENQATDAGESSQSPANQPDMANAADGMQGDDPSAGGQNAGNTAAQG  
 30 ANQAGNNQAAGSSDPIPASNPAPANGGSNFGRVDSLNGVLDGPSQNITLTHCKGDSCSGNNFLDEEVQLKSEF  
 EKLSDADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTS FARFRRSARSRRSLPAEMPLIPVNQAD  
 TLIVDGEAVSLTGHSGNIFAPEGNRYRLTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLFHTENGRP  
 YPTRGRFAAKVDFGSKSVDGIIDSGDDLHMGTKFKAAIDNGFKGTWTENGSGDVSGKFYGPAGEEVAGKSY  
 RPTDAEKGFFGVFAGKKEQD

**SEQ ID 7 – 287-953 hybrid**

MASPDVKSADTLSKPAAPVSEKETEAKEDAPQAGSQGQGAPSQGSQDMAAVSEENTGNGGAAATDKPKNEDE  
 GAQNDMPQNAADTDSLTPNHTPASNMPAGNMENQAPPDAGESEQSPANQPDMANADGMQGDDPSAGGENAGNTAA  
 QGTNQAENNQTAGSQNPASSTNPSATNSGGDFGRTNVGNSVVIDGPSQNITLTHCKGDSCSGNNFLDEEVQLKS  
 EFEKLSDADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTS FARFRRSARSRRSLPAEMPLI  
 40 PVNQADTLIVDGEAVSLTGHSGNIFAPEGNRYRLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLFH  
 TENGRRPSRGRFAAKVDFGSKSVDGIIDSGDLHMGTKFKAAIDNGFKGTWTENGSGDVSGKFYGPAGEEV  
 AGKSYRPTDAEKGFFGVFAGKKEQDGSGGGGATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKR

DGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNGKKLVSDGNLTMHGKTAPVKLKAEK  
FNCYQSPMAKTEVCGGDFTTIDRTKWGVVDYLNVGMTKSVRIDIQIEAAKQ\*

**SEQ ID 8 – 936-741 hybrid**

MVSAGIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETTARSYLRQNNQTKGYTPQISVVGVNRHLLLLGQVATE  
5 GEKQFVGQIARSEQAAEGVNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGI  
LTPEEQAQITQKVSTTVGVQKVITLYQNYVQRGSGGGVAADIGAGLADALTAPLDHKDKGLQSILTLDQSVRKN  
EKLKLAQGAEKTYNGDSLNTGKLNDKVSRFDFIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDS  
EHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDDAGGKLTYTIDFAAKQGNGKIEHLKSPELNV  
DLAAADIKPDGKRHAVISGSVLYNQAEGSYSLGIFGGKAQEVAEVKTVNGIRHIGLAAKQ\*

**SEQ ID 9 – linker**

GSGGGG

**SEQ ID 10 – 741 sequence**

CSSGGGGVAADIGAGLADALTAPLDHKDKGLQSILTLDQSVRKNEKLKLAQGAEKTYNGDSLNTGKLNDKVS  
15 RFDFIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGG  
RATYRGTAFGSDDAGGKLTYTIDFAAKQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEGSY  
SLGIFGGKAQEVAEVKTVNGIRHIGLAAKQ

**SEQ ID 11 – 741 sequence**

CSSGGGGVAADIGAGLADALTAPLDHKDKGLQSILTLDQSVRKNEKLKLAQGAEKTYNGDSLNTGKLNDKVS  
20 RFDFIRQIEVDGQLITLESGEFQIYKQDHSAVVALQIEKINNPDKIDSЛИQRSFLVSGLGGEHTAFNQLPDGK  
AEYHGKAFSSDDAGGKLTYTIDFAAKQGHGKIEHLKTPEQNVELAAELKADEKSHAVILGDTRYGSEEKGTYH  
LALFGDRAQEIAGSATVKIGEKVHEIGIAGKQ

**SEQ ID 12 – 741 sequence**

CSSGGGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEDSIPQNGTLTLSAQGAEKTFKAGDKDNSLNTG  
25 KLKNDKISRFDFVQKIEVDGQQTITLASGEFQIYKQNHSAVVALQIEKINNPDKTDSLINQRSFLVSGLGGEHTA  
FNQLPGGKAEYHGKAFSSDDPNGLHYSIDFTKKQGYGRIEHLKTLEQNVELAAELKADEKSHAVILGDTRYG  
SEEKGTYHLALFGDRAQEIAGSATVKIGEKVHEIGIAGKQ